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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=8; day=11; hr=14; min=16; sec=4; ms=564;]

=====

Reviewer Comments:

<210> 2

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> peptide construct

The above <223> response is an insufficient explanation for "<213> Artificial Sequence." Please give the source of the genetic material.

<210> 6

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Completely synthesized peptide construct

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> cyclohexylalanine, D-alanine, acetyl, ClAc, BrAc

<220>

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<222> (1)..(1)

<223> Xaa is an amino acid V, L, I, G or A

<220>
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<222> (5)..(5)
<223> Xaa is an amino acid V, L, I, G or A

<220>
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<400> 6

Xaa Glu Glu Thr Xaa Gly Xaa Ser Gln Leu Glu Val Gly Gly Gly

Sequence 6 above shows no amino acid numbers: please insert them under every 5 amino acids. Do not use TAB codes between the amino acid numbers: they cause misalignment. Same error in Sequence 29.

<210> 21
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
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<222> (7)..(8)
<223> gamma aminobutyric acid (gaba) or 3 amino propanoic acid (apa)

<220>
<221> MOD_RES
<222> (17)..(17)
<223> AMIDATION

<400> 21

Asp	Gly	Gln	Glu	Glu	Lys	Ala	Val	Val	Ser	Thr	Gly	Leu	Ile	Gly	Gly
1				5					10					15	

Gly

The above <220>-<223> section describing amino acids at locations 7 and 8 is incorrect: "Ala" is at location 7 and can only represent itself: "Val" is at location 8 and can only represent itself. They cannot represent "GABA" or "apa." Please use "Xaa's" instead, at locations 7 and 8, and explain in the <220>-<223> section. This type of error also appears in subsequent sequences.

Application No: 10502328 Version No: 4.0

Input Set:**Output Set:**

Started: 2008-07-03 14:21:05.491
Finished: 2008-07-03 14:21:26.826
Elapsed: 0 hr(s) 0 min(s) 21 sec(s) 335 ms
Total Warnings: 29
Total Errors: 23
No. of SeqIDs Defined: 29
Actual SeqID Count: 29

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (2)
E 257	Invalid sequence data feature in <221> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
E 257	Invalid sequence data feature in <221> in SEQ ID (3)
E 257	Invalid sequence data feature in <221> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
E 257	Invalid sequence data feature in <221> in SEQ ID (7)
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W 213	Artificial or Unknown found in <213> in SEQ ID (9)
E 257	Invalid sequence data feature in <221> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
E 257	Invalid sequence data feature in <221> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
E 257	Invalid sequence data feature in <221> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)

Input Set:

Output Set:

Started: 2008-07-03 14:21:05.491
Finished: 2008-07-03 14:21:26.826
Elapsed: 0 hr(s) 0 min(s) 21 sec(s) 335 ms
Total Warnings: 29
Total Errors: 23
No. of SeqIDs Defined: 29
Actual SeqID Count: 29

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (13)
E 257	Invalid sequence data feature in <221> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
E 257	Invalid sequence data feature in <221> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
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W 213	Artificial or Unknown found in <213> in SEQ ID (16)
E 257	Invalid sequence data feature in <221> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
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W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20) This error has occurred more than 20 times, will not be displayed
E 257	Invalid sequence data feature in <221> in SEQ ID (20)
E 257	Invalid sequence data feature in <221> in SEQ ID (21)
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E 257	Invalid sequence data feature in <221> in SEQ ID (23)
E 257	Invalid sequence data feature in <221> in SEQ ID (25)
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SEQUENCE LISTING

<110> Zimmerman, Daniel H
 Charoenvit, Yupin
 Rosenthal, Kenneth
 Whelan, Mike

<120> METHODS FOR TREATING DISEASES OR CONDITIONS WITH PEPTIDE
 CONSTRUCTS

<130> CS-118

<140> 10502328
 <141> 2005-05-19

<150> US 60/350,032
 <151> 2002-01-23

<150> US 60/349,982
 <151> 2002-01-23

<150> US 60/349,983
 <151> 2002-01-23

<150> PCT/US03/01816
 <151> 2003-01-23

<160> 29

<170> PatentIn version 3.2

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<220>
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<223> acetyl, ClAc, BrAc

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<223> X is A or N and when X is A, then A is either cyclohexylalanine or D-alanine

<220>
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<223> highly variable fragment wherein isoleucine at 143 and leucine at 159 in contact with CD4 phenylalanine as the 43 residue

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<400> 2

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1				5				10					15	

<210> 3
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<220>
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1 5 10

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Asn Gly Gln Glu Glu Thr Val Gly Val Ser Ser Thr Gln Leu Ile
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<210> 5

<211> 18

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Asn Gly Gln Glu Glu Lys Ala Gly Val Val Ser Thr Gly Leu Ile Gly
1 5 10 15

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<210> 6

<211> 15

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<222> (1)..(1)

<223> cyclohexylalanine, D-alanine, acetyl, ClAc, BrAc

<220>

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<223> Xaa is an amino acid V, L, I, G or A

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<223> Xaa is an amino acid V, L, I, G or A

<220>
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<223> Xaa is an amino acid V, L, I, G or A

<400> 6

Xaa Glu Glu Thr Xaa Gly Xaa Ser Gln Leu Glu Val Gly Gly Gly

<210> 7
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<220>
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1 5 10 15

Gly Gly

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1 5 10 15

Gly

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<223> acetyl, ClAc, BrAc

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<220>
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Lysine or hydroxy-Leucine or Leucine

<220>
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Xaa Gly Gln Glu Glu Xaa Ala Gly Val Val Ser Thr Gly Leu Ile Gly
1 5 10 15

Gly Gly

<210> 10
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Gly Gly

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<210> 12
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<220>

<221> MOD_RES

<222> (10)..(10)

<223> AMIDATION

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1 5 10

<210> 13

<211> 9

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<223> acetyl, ClAc, BrAc

<220>

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<220>

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1 5

<210> 14

<211> 8

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1 5

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1 5

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<223> X is A or E and when X is A, then A is either cyclohexylalanine or D-alanine

<220>
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<222> (6)..(6)
<223> AMIDATION

<400> 16

Xaa Thr Val Gly Val Ser
1 5

<210> 17
<211> 5
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Xaa Thr Val Gly Val
1 5

<210> 18
<211> 15

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 <223> acetyl, ClAc, BrAc

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 <400> 18

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1				5				10					15	

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 <400> 19

Xaa	Gln	Glu	Glu	Lys	Ala	Gly	Val	Val	Ser	Thr	Gly	Leu	Ile
1				5				10					

<210> 20
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<220>
<221> MOD_RES
<222> (19)..(19)
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<400> 20

Xaa Gly Gln Glu Glu Lys Ala Gly Gly Val Val Ser Thr Gly Leu Ile
1 5 10 15

Gly Gly Gly

<210> 21
<211> 17
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<400> 21

Asp Gly Gln Glu Glu Lys Ala Val Val Ser Thr Gly Leu Ile Gly Gly
1 5 10 15

Gly

<210> 22
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 <223> GG is replaced with gamma aminobutyric acid (gaba) or 3 amino
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 <400> 22

Xaa Gly Gln Glu Ala Gly Val Val Ser Thr Gly Leu Ile Gly Gly Gly
 1 5 10 15

<210> 23
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1 5 10 15

<210> 24
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<400> 24

Xaa Gly Gln Glu Glu Lys Ala Gly Val Val Ser Thr Gly Leu Ile Gln
1 5 10 15

Asn Gly Asp Trp Thr Phe Gln Thr Leu Val
20 25

<210> 25
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<222> (26)..(26)
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Asp Gly Asp Trp Thr Phe Gln Thr Leu Val
20 25

<210> 26
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<222> (18)..(18)
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<223> S or not present

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<223> AMIDATION

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1 5 10 15

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20 25

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<220>

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<222> (22)..(22)

<223> AMIDATION

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1 5 10 15

Thr Phe Gln Thr Leu Val
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<210> 28
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 1 5 10 15

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<223> AMIDATION

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Xaa Val Ala Lys Glu